

SEQUENCE LISTING

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Topouzis, Stavros
Gilbertson, Debra G.

<120> METHOD OF TREATING FIBROPROLIFERATIVE
DISORDERS

<130> 00-79

<150> US 60/235,295

<151> 2000-09-26

<150> US 09/564,595

<151> 2000-05-03

<150> US 60/180,169

<151> 2000-02-04

<150> US 60/164,463

<151> 1999-11-10

<150> US 60/132,250

<151> 1999-05-03

<160> 13

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1882

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (226)...(1338)

<400> 1

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gttcagcatg caggaagttt ggggagagct cggcgattag cacagcgacc cgggccagcg      120
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cagggcgagc gcaggcgggc agagcgcagg gcggcgcggc gtcggtcccg ggagcagaac 180
 ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc 237
 Met His Arg Leu

1

atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac 285
 Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp
 5 10 15 20

act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc 333
 Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala
 25 30 35

aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga 381
 Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg
 40 45 50

gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga 429
 Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg
 55 60 65

ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac 477
 Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His
 70 75 80

tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga 525
 Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly
 85 90 95 100

tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt 573
 Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val
 105 110 115

gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga 621
 Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly
 120 125 130

cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa 669
 His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys
 135 140 145

atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys 150 155 160	717
att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu 165 170 175 180	765
acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn 185 190 195	813
tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys 200 205 210	861
aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn 215 220 225	909
cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro 230 235 240	957
cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu 245 250 255 260	1005
gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn 265 270 275	1053
tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe 280 285 290	1101
ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys 295 300 305	1149
gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val 310 315 320	1197

aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg 1245
 Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg
 325 330 335 340

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293
 Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
 345 350 355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338
 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg agggtgagat 1398
 aagagaccct ttctctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458
 agtggttgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatatca 1518
 tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga ggttatatat 1578
 gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaaaa tgtttttttt 1638
 ttttggtata tataaccagg tacaccagag gttacatatg ttgagttag actcttaaaaa 1698
 tcctttgccaa aaataaggga tgggtcaaata tatgaaacat gtcttttagaa aatttaggag 1758
 ataaatttat ttttaaatTT tgaacacga aacaattttg aatcttgctc tcttaaagaa 1818
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 tatt 1882

<210> 2

<211> 370

<212> PRT

<213> Homo sapiens

<400> 2

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
 1 5 10 15
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 20 25 30
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
 35 40 45
 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
 50 55 60
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 65 70 75 80
 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
 85 90 95

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 100 105 110
 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
 115 120 125
 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
 130 135 140
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
 180 185 190
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
 195 200 205
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
 225 230 235 240
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
 275 280 285
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 325 330 335
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
 355 360 365
 Pro Arg
 370

<210> 3

<211> 1472

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (93)...(1205)

<400> 3

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gagcaacgcg atccctaggt cgctgagccc aa atg caa cgg ctc gtt tta gtc      113
                               Met Gln Arg Leu Val Leu Val
                               1                               5

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tcc att ctc ctg tgc gcg aac ttt agc tgc tat ccg gac act ttt gcg      161
Ser Ile Leu Leu Cys Ala Asn Phe Ser Cys Tyr Pro Asp Thr Phe Ala
          10                      15                      20

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act ccg cag aga gca tcc atc aaa gct ttg cgc aat gcc aac ctc agg      209
Thr Pro Gln Arg Ala Ser Ile Lys Ala Leu Arg Asn Ala Asn Leu Arg
          25                      30                      35

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aga gat gag agc aat cac ctc aca gac ttg tac cag aga gag gag aac      257
Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Gln Arg Glu Glu Asn
          40                      45                      50                      55

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att cag gtg aca agc aat ggc cat gtg cag agt cct cgc ttc ccg aac      305
Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro Asn
          60                      65                      70

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```

agc tac cca agg aac ctg ctt ctg aca tgg tgg ctc cgt tcc cag gag      353
Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln Glu
          75                      80                      85

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aaa aca cgg ata caa ctg tcc ttt gac cat caa ttc gga cta gag gaa      401
Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu Glu
          90                      95                      100

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gca gaa aat gac att tgt agg tat gac ttt gtg gaa gtt gaa gaa gtc      449
Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Glu Val
          105                      110                      115

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tca gag agc agc-act gtt gtc aga gga aga tgg tgt ggc cac aag gag      497
Ser Glu Ser Ser Thr Val Val Arg Gly Arg Trp Cys Gly His Lys Glu
          120                      125                      130                      135

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atc cct cca agg ata acg tca aga aca aac cag att aaa atc aca ttt Ile Pro Pro Arg Ile Thr Ser Arg Thr Asn Gln Ile Lys Ile Thr Phe 140 145 150	545
aag tct gat gac tac ttt gtg gca aaa cct gga ttc aag att tat tat Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr Tyr 155 160 165	593
tca ttt gtg gaa gat ttc caa ccg gaa gca gcc tca gag acc aac tgg Ser Phe Val Glu Asp Phe Gln Pro Glu Ala Ala Ser Glu Thr Asn Trp 170 175 180	641
gaa tca gtc aca agc tct ttc tct ggg gtg tcc tat cac tct cca tca Glu Ser Val Thr Ser Ser Phe Ser Gly Val Ser Tyr His Ser Pro Ser 185 190 195	689
ata acg gac ccc act ctc act gct gat gcc ctg gac aaa act gtc gca Ile Thr Asp Pro Thr Leu Thr Ala Asp Ala Leu Asp Lys Thr Val Ala 200 205 210 215	737
gaa ttc gat acc gtg gaa gat cta ctt aag cac ttc aat cca gtg tct Glu Phe Asp Thr Val Glu Asp Leu Leu Lys His Phe Asn Pro Val Ser 220 225 230	785
tgg caa gat gat ctg gag aat ttg tat ctg gac acc cct cat tat aga Trp Gln Asp Asp Leu Glu Asn Leu Tyr Leu Asp Thr Pro His Tyr Arg 235 240 245	833
ggc agg tca tac cat gat cgg aag tcc aaa gtg gac ctg gac agg ctc Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu 250 255 260	881
aat gat gat gtc aag cgt tac agt tgc act ccc agg aat cac tct gtg Asn Asp Asp Val Lys Arg Tyr Ser Cys Thr Pro Arg Asn His Ser Val 265 270 275	929
aac ctc agg gag gag ctg aag ctg acc aat gca gtc ttc ttc cca cga Asn Leu Arg Glu Glu Leu Lys Leu Thr Asn Ala Val Phe Phe Pro Arg 280 285 290 295	977
tgc ctc ctc gtg cag cgc tgt ggt ggc aac tgt ggt tgc gga act gtc Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val 300 305 310	1025

aac tgg aag tcc tgc aca tgc agc tca ggg aag aca gtg aag aag tat 1073
 Asn Trp Lys Ser Cys Thr Cys Ser Ser Gly Lys Thr Val Lys Lys Tyr
 315 320 325

cat gag gta ttg aag ttt gag cct gga cat ttc aag aga agg ggc aaa 1121
 His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly Lys
 330 335 340

gct aag aat atg gct ctt gtt gat atc cag ctg gat cat cat gag cga 1169
 Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg
 345 350 355

tgt gac tgt atc tgc agc tca aga cca cct cga taa aacactatgc 1215
 Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

acatctgtac ttgtattatg aaaggacctt taggttacia aaaccctaag aagcttctaa 1275
 tctcagtga atgaatgcat atggaaatgt tgctttgtta gtgccatggc aagaagaagc 1335
 aaatatcatt aatttctata tacataaaca taggaattca cttatcaata gtatgtgaag 1395
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 attcagtata ttactg 1472

<210> 4

<211> 370

<212> PRT

<213> Mus musculus

<400> 4

Met Gln Arg Leu Val Leu Val Ser Ile Leu Leu Cys Ala Asn Phe Ser
 1 5 10 15
 Cys Tyr Pro Asp Thr Phe Ala Thr Pro Gln Arg Ala Ser Ile Lys Ala
 20 25 30
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
 35 40 45
 Leu Tyr Gln Arg Glu Glu Asn Ile Gln Val Thr Ser Asn Gly His Val
 50 55 60
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 65 70 75 80
 Trp Trp Leu Arg Ser Gln Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp
 85 90 95
 His Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 100 105 110

Phe Val Glu Val Glu Glu Val Ser Glu Ser Ser Thr Val Val Arg Gly
 115 120 125
 Arg Trp Cys Gly His Lys Glu Ile Pro Pro Arg Ile Thr Ser Arg Thr
 130 135 140
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Phe Val Glu Asp Phe Gln Pro Glu
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Phe Ser Gly
 180 185 190
 Val Ser Tyr His Ser Pro Ser Ile Thr Asp Pro Thr Leu Thr Ala Asp
 195 200 205
 Ala Leu Asp Lys Thr Val Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys His Phe Asn Pro Val Ser Trp Gln Asp Asp Leu Glu Asn Leu Tyr
 225 230 235 240
 Leu Asp Thr Pro His Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Val Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn His Ser Val Asn Leu Arg Glu Glu Leu Lys Leu Thr
 275 280 285
 Asn Ala Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Lys Ser Cys Thr Cys Ser Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Lys Phe Glu Pro Gly
 325 330 335
 His Phe Lys Arg Arg Gly Lys Ala Lys Asn Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
 355 360 365
 Pro Arg
 370

<210> 5

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer ZC21,987

<400> 5
caacctgttg ttgtcccgt cacc 24

<210> 6
<211> 24
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<212> DNA
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<223> oligonucleotide primer ZC26317

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Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln
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 Ile Lys

<210> 10

<211> 25

<212> PRT

<213> Artificial Sequence

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<400> 10

Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg
 1 5 10 15
 Tyr Arg Gly Arg Ser Tyr His Asp Cys
 20 25

<210> 11

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 11

Cys Phe Glu Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met
 1 5 10 15
 Ala Leu Val Asp Ile Gln Leu Asp
 20

<210> 12

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 12

Glu Tyr Met Pro Met Glu

1

5

<210> 13

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> peptide

<400> 13

Glu Tyr Met Pro Thr Asp

1

5